

Table 3

5'	9	18	27	36	45	54											
NNN	NGC	CAN	GCC	CAA	AGC	CCT	GGT	ACC	CGC	GCG	GTG	GGG	CCT	CAG	TCT	GCG	GCC
	63	72	81	90	99	108											
ATG	GGG	GCG	TCC	GCG	CTG	CTG	CGA	GCG	GTG	ATC	ATG	GGG	GCC	CCG	GGC	TCG	
M	G	A	S	A	R	L	L	R	A	V	I	M	G	A	P	G	S
	117	126	135	144	153	162											
GGC	AAG	GCG	ACC	GTG	TCG	TCG	CGC	ATC	ACT	ACA	CAC	TTC	GAG	CTG	AAG	CAC	CTC
G	K	G	T	V	S	S	R	I	T	T	H	F	E	L	K	H	L
	171	180	189	198	207	216											
TCC	AGC	GGG	GAC	CTG	CTC	CGG	GAC	AAC	ATG	CTG	CGG	GGC	ACA	GAA	ATT	GGC	GTG
S	S	G	D	L	L	R	D	N	M	L	R	G	T	E	I	G	V
	225	234	243	252	261	270											
TTA	GCC	AAG	GCT	TTC	ATT	GAC	CAA	GGG	AAA	CTC	ATC	CCA	GAT	GAT	GTC	ATG	ACT
L	A	K	A	F	I	D	Q	G	K	L	I	P	D	D	V	M	T
	279	288	297	306	315	324											
CGG	CTG	GCC	CTT	CAT	GAG	CTG	AAA	AAT	CTC	ACC	CAG	TAT	AGC	TGG	CTG	TTG	GAT
R	L	A	L	H	E	L	K	N	L	T	Q	Y	S	W	L	L	D

FIGURE 1A

Table 1B

333	342	351	360	369	378
GGT TTT CCA AGG ACA CTT CCA CAG GCA GAA GCC CTA GAT AGA GCT TAT CAG ATC					
G F P R T L P Q A E A L D R A Y Q I					
387	396	405	414	423	432
GAC ACA GTG ATT AAC CTG AAT GTG CCC TTT GAG GTC ATT AAA CAA CGC CTT ACT					
D T V I N L N V P F E V I K Q R L T					
441	450	459	468	477	486
GCT CGC TGG ATT CAT CCC GCC AGT GGC CGA GTC TAT AAC ATT GAA TTC AAC CCT					
A R W I H P A S G R V Y N I E F N P					
495	504	513	522	531	540
CCC AAA ACT GTG GGC ATT GAT GAC CTG ACT GGG GAG CCT CTC ATT CAG CGT GAG					
P K T V G I D D L T G E P L I Q R E					
549	558	567	576	585	594
GAT GAT AAA CCA GAG ACG GTT ATC AAG AGA CTA AAG GCT TAT GAA GAC CAA ACA					
D D K P E T V I K R L K A Y E D Q T					
603	612	621	630	639	648
AAG NCA GTC CTG GNA TAT TAC CAG AAA AAA GGG GTG CTG GAA ACA TTC TCC GGA					
K X V L X Y Y Q K K G V L E T F S G					

FIGURE 1B

Figure 1C

657	666	675	684	693	702
ACA GAA ACC AAC AAG ATT TGG CCC TAT GTA TAT GCT TTC CTA CAA ACT AAA GTT					
T E T N K I W P Y V Y A F L Q T K V					
711	720	729	738	747	756
CCA CAA AGA AGC CAG AAA GCT TCA GTT ACT CCA TGA GGA GAA ATG TGT GTA ACT					
P Q R S Q K A S V T P					
765	774	783	792	801	810
ATT AAT AGT AAG ATG GGC AAA CCT CCT AGT AGT CCT TGC ATT TAG AAG CTG CTT TTC					
819	828	837	846	855	
CTA AGA CTT CTA GTA TGT ATG AAT TCT TTG AAA ATT ATA TTA CTT TTA 3'					

FIGURE 1C

1	M	G	A	S	A	R	L	L	R	A	V	I	M	G	A	P	G	S	G	K	G	T	V	S	S	R	I	T	H	F	E	L	K	H	L	S	S	G	D	HMAK	
1	M	G	A	S	A	R	L	L	R	A	A	I	M	G	A	P	G	S	G	K	G	T	V	S	S	R	I	T	K	H	F	E	L	K	H	L	S	S	G	D	g217576
1	M	G	A	S	G	R	L	L	R	A	V	I	M	G	A	P	G	S	G	K	G	T	G	S	S	R	I	T	K	H	F	E	L	K	H	L	S	S	G	D	g450312
1	M	A	S	-	-	K	L	L	R	A	V	I	L	G	P	P	G	S	G	K	G	T	V	C	Q	R	I	A	Q	N	F	G	L	Q	H	L	S	S	G	H	g28577
41	L	L	R	D	N	M	L	R	G	T	E	I	G	V	L	A	K	A	F	I	D	Q	G	K	L	I	P	D	D	V	M	T	R	L	A	L	H	E	L	K	HMAK
41	L	L	R	D	N	M	L	R	G	T	E	I	G	V	L	A	K	T	F	I	D	Q	G	K	L	I	P	D	D	V	M	T	R	L	V	L	H	E	L	K	g217576
41	L	L	R	Q	N	M	L	Q	G	T	E	I	A	V	L	A	K	S	F	I	D	Q	G	K	L	I	P	D	D	D	M	T	R	L	A	L	H	E	L	K	g450312
39	F	L	R	E	N	I	K	A	S	T	E	V	G	E	M	A	K	Q	Y	I	E	K	S	L	L	V	P	D	H	V	I	T	R	L	M	M	S	E	L	E	g28577
81	N	L	T	Q	Y	S	W	L	L	D	G	F	P	R	T	L	P	Q	A	E	A	L	D	R	A	Y	Q	I	D	T	V	I	N	L	N	V	P	F	E	V	HMAK
81	N	L	T	Q	Y	N	W	L	L	D	G	F	P	R	T	L	P	Q	A	E	A	L	D	R	A	Y	Q	I	D	T	V	I	N	L	N	V	P	F	E	V	g217576
81	N	L	T	Q	C	S	W	L	L	D	G	F	P	R	T	L	P	Q	A	E	A	L	D	R	V	Y	Q	I	D	T	V	I	N	L	N	V	P	F	E	V	g450312
79	N	R	R	G	Q	H	W	L	L	D	G	F	P	R	T	L	G	Q	A	E	A	L	D	K	I	C	E	V	D	L	V	I	S	L	N	I	P	F	E	T	g28577

FIGURE 2A

121	I	K	Q	R	L	T	A	R	W	I	H	P	A	S	G	R	V	Y	N	I	E	F	N	P	P	K	T	V	G	I	D	D	L	T	G	E	P	L	I	Q	HMAK			
121	I	K	Q	R	L	T	A	R	W	I	H	P	G	S	G	R	V	Y	N	I	E	F	N	P	P	K	T	M	G	I	D	D	L	T	G	E	P	L	V	Q	g217576			
121	I	K	L	R	L	T	A	R	W	I	H	P	A	S	G	R	V	Y	N	I	E	F	N	P	P	K	T	V	G	I	D	D	L	T	G	E	P	L	I	Q	g450312			
119	L	K	D	R	L	S	R	R	W	I	H	P	P	S	G	R	V	Y	N	L	D	F	N	P	P	H	V	H	G	I	D	D	V	T	G	E	P	L	V	Q	g28577			
161	R	E	D	D	K	P	E	T	V	I	K	R	L	K	A	Y	E	D	Q	T	K	X	V	L	X	Y	Y	Q	K	K	G	V	L	E	T	F	S	G	T	E	HMAK			
161	R	E	D	D	R	P	E	T	V	V	K	R	L	K	A	Y	E	A	Q	T	E	P	V	L	E	Y	Y	R	K	K	G	V	L	E	T	F	S	G	T	E	g217576			
161	R	E	D	D	K	P	E	T	V	I	K	R	L	K	A	Y	E	A	Q	T	E	P	V	L	Q	Y	Y	Q	K	K	G	V	L	E	T	F	S	G	T	E	g450312			
159	Q	E	D	D	K	P	E	A	V	A	A	R	L	R	Q	Y	K	D	V	A	K	P	V	I	E	L	Y	K	S	R	G	V	L	H	Q	F	S	G	T	E	g28577			
201	T	N	K	I	W	P	Y	V	Y	A	F	L	Q	T	K	V	P	Q	R	S	Q	K	A	S	V	T	P																	HMAK
201	T	N	K	I	W	P	H	V	Y	A	F	L	Q	T	K	L	P	Q	R	S	Q	E	T	S	V	T	P														g217576			
201	T	N	K	I	R	P	H	V	Y	S	F	L	Q	M	K	V	P	E	T	I	Q	K	A	S	V	T	P														g450312			
199	T	N	K	I	W	P	Y	V	Y	T	L	F	S	N	K	I	T	P	I	Q	S	K	E	A	Y																g28577			

FIGURE 2B

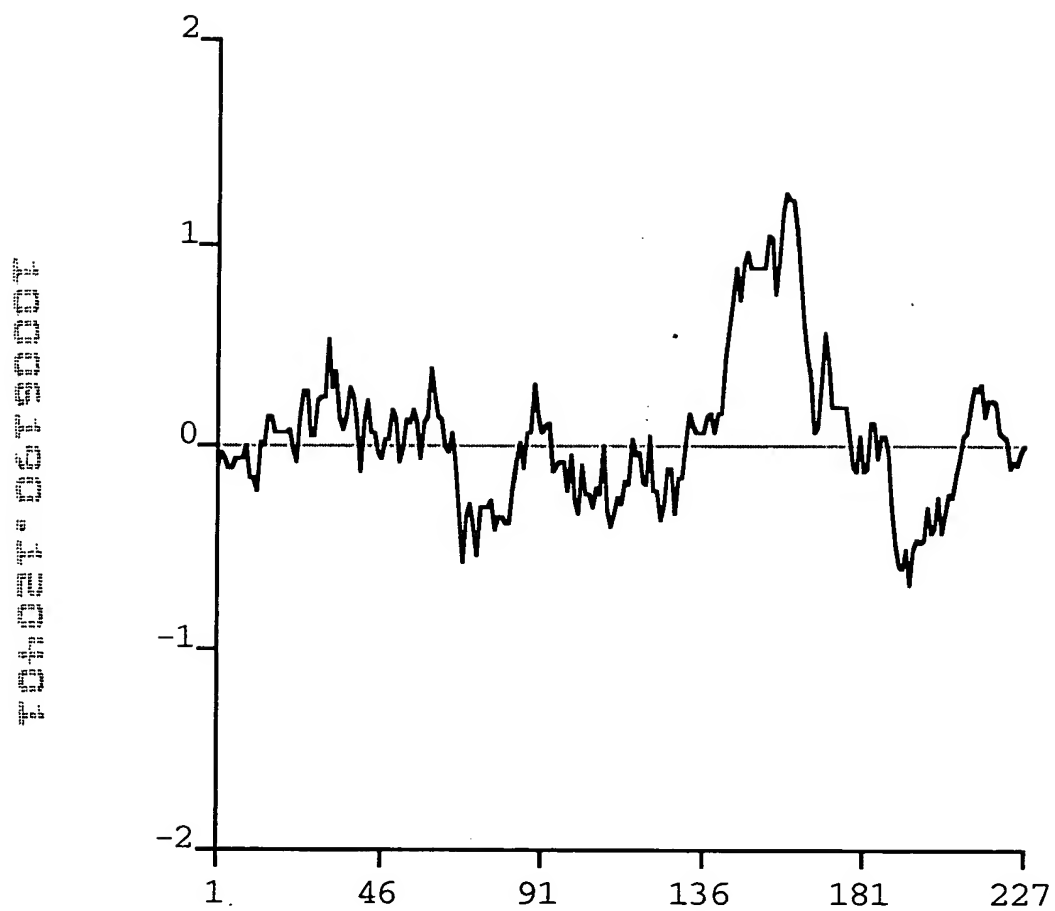


FIGURE 3A

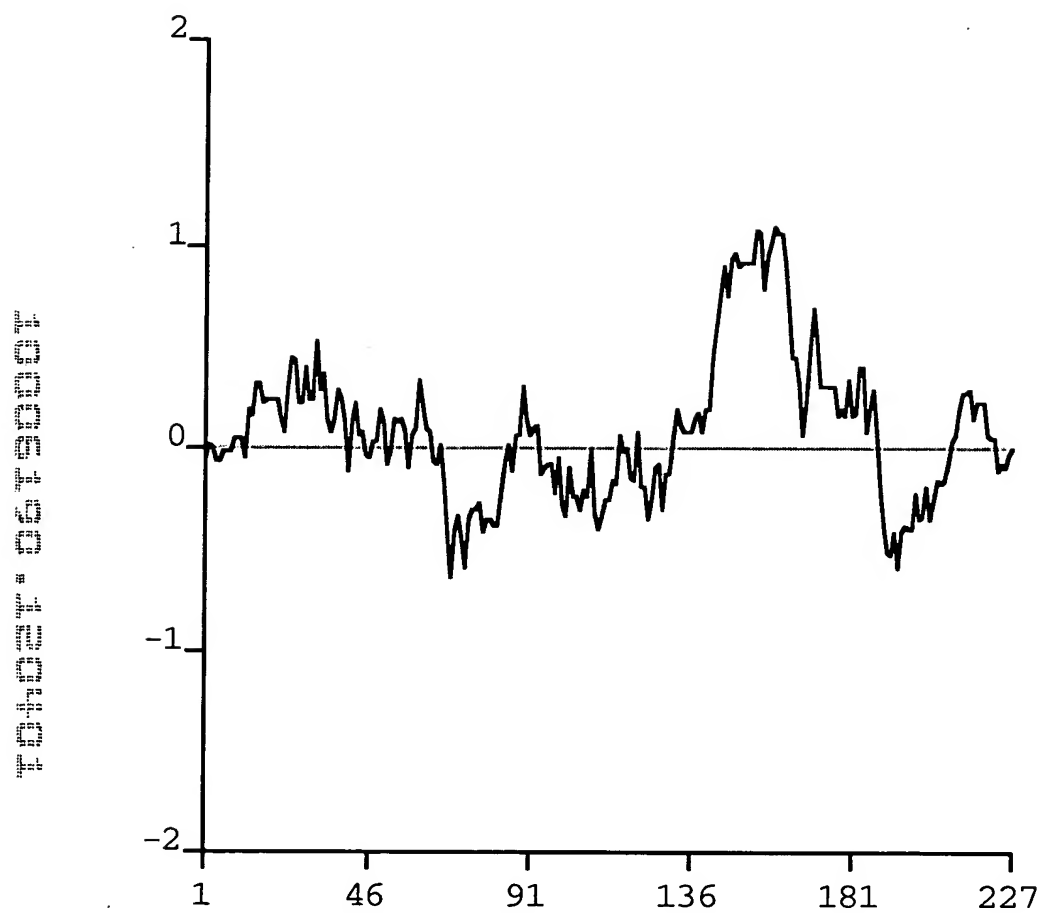


FIGURE 3B

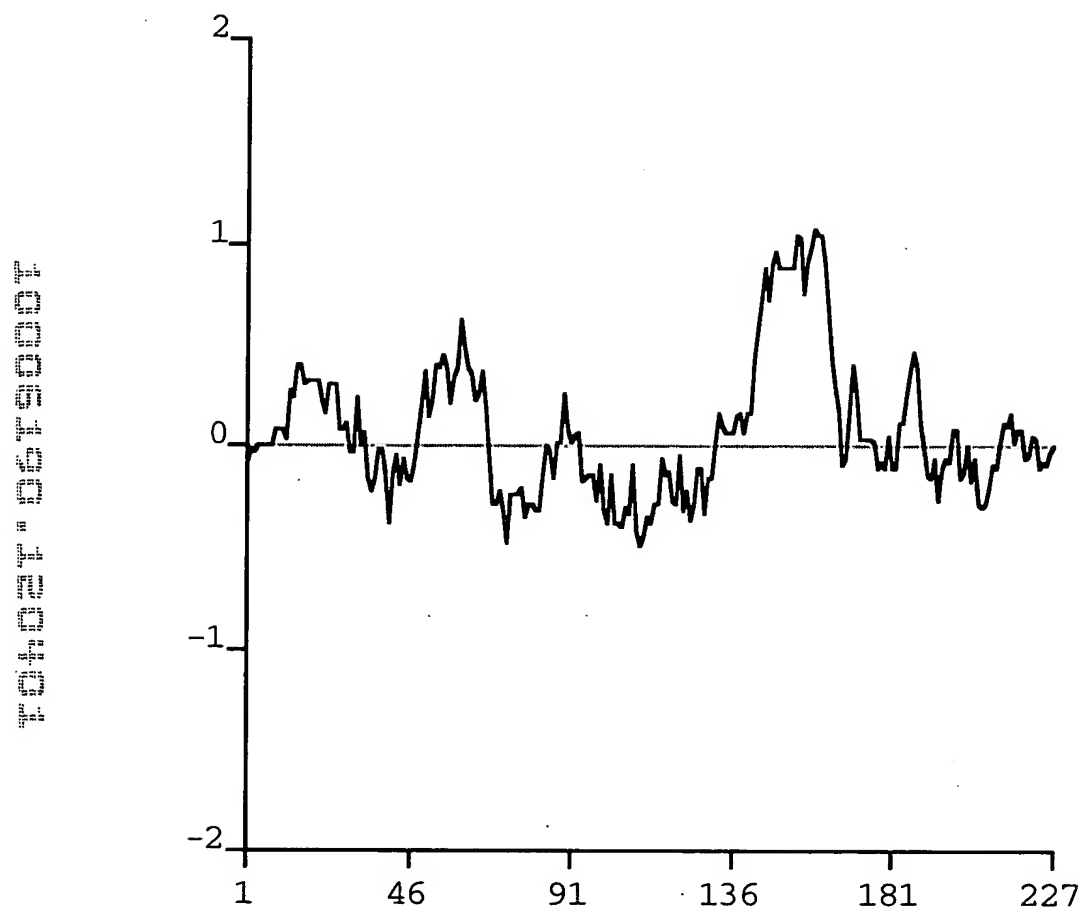


FIGURE 3C

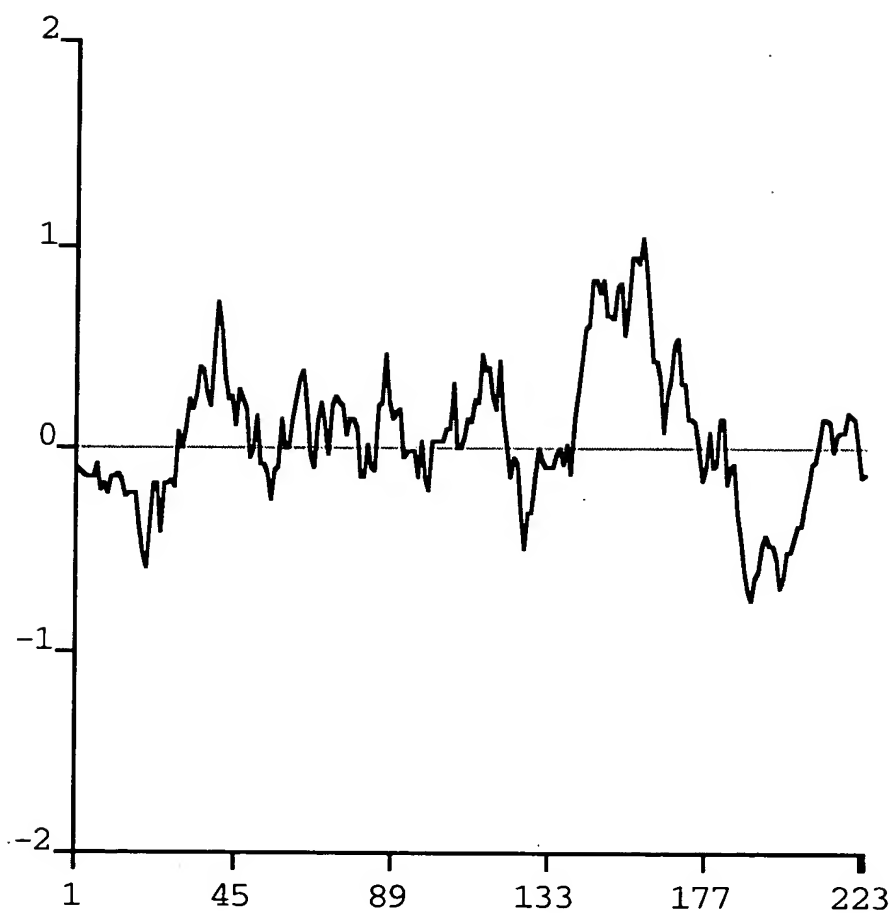


FIGURE 3D

Library	Lib Description	Abun	Pct Abun
MUSCNOT01	muscle, skeletal	2	0.0890
COLNNOT07	colon, 60 M, match to COLNTUT16	1	0.0409
SEMVNOT01	seminal vesicle, 58 M	1	0.0272
COLNTUT16	colon tumor, 60 M, match to COLNNOT07/08/09/11	1	0.0256
SKINBIT01	skin, leg, erythema nodosum	1	0.0256
OVARTUT04	ovarian tumor, 53 F	1	0.0252
ADRENOT08	adrenal gland, 20 M	1	0.0249
LIVSFEM03	liver/spleen, fetal M, NORM, WM	1	0.0246
HIPOAZT01	brain, hippocampus, Alzheimer's, 74 M	1	0.0245
TMLR2DT01	lymphocytes (non-adher PBMNC), M/F, 24-hr MLR	1	0.0212
SYNORAB01	synovium, hip, rheumatoid, 68 F	1	0.0195
HNT2RAT01	hNT2 cell line, teratocarcinoma, treated RA	1	0.0188
BRSTNOT07	breast, 43 F	1	0.0146
PLACNOM02	placenta, neonatal F, NORM, WM	2	0.0111
NGANNOT01	ganglioneuroma, 9 M	1	0.0073
LIVSFEM02	liver/spleen, fetal M, NORM, WM	1	0.0026

Electronic Northern Results returned a total of 16 row(s).

FIGURE 4